

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2000, 10:15:10 : Search time 10069.4 Seconds
(without alignments)
3787.874 Million cell updates/sec

Title: US-09-227-881-3

Perfect score: 6169

Sequence: 1 atcttgtagctgaattacctc.....ctgtgccccctccatgtcag 6169

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
15: gb_est15:*
16: gb_est16:*
17: gb_est17:*
18: gb_est18:*
19: gb_est19:*
20: gb_est20:*
21: gb_est21:*
22: gb_est22:*
23: gb_est23:*
24: gb_est24:*
25: gb_est25:*
26: gb_est26:*
27: gb_est27:*
28: gb_est28:*
29: gb_est29:*
30: gb_est30:*
31: gb_est31:*
32: gb_est32:*
33: gb_est33:*
34: gb_est34:*
35: gb_est35:*
36: gb_est36:*
37: gb_est37:*
38: gb_est38:*
39: gb_est39:*
40: gb_est40:*
41: em_est4a:*
42: em_estfun:*
43: em_esthum1:*

44: em_esthum2:*
45: em_esthum3:*
46: em_esthum4:*
47: em_esthum5:*
48: em_esthum6:*
49: em_esthum7:*
50: em_esthum8:*
51: em_esthum9:*
52: em_esthum10:*
53: em_esthum11:*
54: em_esthum12:*
55: em_esthum13:*
56: em_esthum14:*
57: em_esthum15:*
58: em_esthum16:*
59: em_esthum17:*
60: em_esthum18:*
61: em_esthum19:*
62: em_esthum20:*
63: em_estin1:*
64: em_estin2:*
65: em_estin3:*
66: em_estin4:*
67: em_estom:*
68: em_estov1:*
69: em_estov2:*
70: em_estp1:*
71: em_estp12:*
72: em_estp13:*
73: em_estp14:*
74: em_estp15:*
75: em_estro1:*
76: em_estro2:*
77: em_estro3:*
78: em_estro4:*
79: em_estro5:*
80: em_estro6:*
81: em_estro7:*
82: em_estro8:*
83: em_estro9:*
84: em_estro10:*
85: em_estro11:*
86: em_estro12:*
87: em_estro13:*
88: gb_gss1:*
89: gb_gss2:*
90: gb_gss3:*
91: gb_gss4:*
92: em_gss1:*
93: em_gss2:*
94: em_gss3:*
95: em_gss4:*
96: gb_gss5:*
97: gb_gss6:*
98: gb_gss7:*
99: gb_gss8:*
100: gb_gss9:*
101: gb_gss10:*
102: gb_gss11:*
103: gb_gss12:*
104: gb_gss13:*
105: gb_gss14:*
106: gb_gss15:*
107: gb_gss16:*
108: gb_gss17:*
109: gb_gss18:*
110: gb_gss19:*
111: gb_gss20:*
112: gb_gss21:*
113: gb_gss22:*
114: gb_gss23:*
115: gb_gss24:*
116: em_gss5:*

117: em_gss6:*
118: em_gss7:*
119: em_gss8:*
120: em_gss9:*
121: em_gss10:*
122: em_gss11:*
123: em_gss12:*
124: em_gss13:*
125: em_gss14:*
126: em_gss15:*
127: em_gss16:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	180.8	2.9	660	88	A0057239 CIT-HSP-2
2	179.8	2.9	539	96	A0379787 RPCI1-115
3	179	2.9	645	100	A0636457 RPCI-11-4
4	179	2.9	678	96	A0387027 RPCI1-15
5	178.4	2.9	537	25	AM978041 EST390150
6	177.6	2.9	516	89	A0112451 CIT-HSP-2
7	177.4	2.9	577	91	A0265389 CITR1-E1
8	177.2	2.9	548	11	A1583291 CITR1-E1
9	176.6	2.9	434	90	A0199435 RPCI1-158
10	176.6	2.9	591	25	AM979191 EST391301
11	176	2.9	521	21	AM273360 x138a04.x
12	176	2.9	551	39	T53829 yb85d10.s1
13	175.8	2.8	589	91	A0283440 RPCI1-79
14	175.4	2.8	386	98	A0474222 CITR1-E1
15	175.2	2.8	711	97	A0415030 RPCI-11-2
16	175	2.8	388	19	AM069227 CT41h09.x
17	175	2.8	421	23	AM674631 bd41a11.x
18	175	2.8	447	24	AM820784 RC3-ST030
19	175	2.8	454	12	A1634187 t555a08.x
20	175	2.8	474	10	A1457313 CT13a05.x
21	175	2.8	527	11	A1523813 t996d09.x
22	174.8	2.8	432	9	A1300818 qn47c06.x
23	174.6	2.8	435	9	A1310892 q095a06.x
24	174.6	2.8	424	10	A1431513 t45f04.x
25	174.6	2.8	677	110	B6612 CIT-HSP-201
26	174.2	2.8	342	6	AA846823 oe08d01.s
27	173.8	2.8	460	110	B15692 345N8.TP.CT
28	173.8	2.8	565	25	AM953220 EST365290
29	173.6	2.8	368	21	AM270385 xp74f06.x
30	173.6	2.8	374	37	F35684 HSPD32531.H
31	173.4	2.8	384	7	AA862029 o146e04.s
32	173.4	2.8	427	5	AA550889 nj35d12.s
33	173.4	2.8	436	88	A0021084 CIT-HSP-2
34	173.4	2.8	486	8	A1049955 an38e01.x
35	173.4	2.8	642	110	B59854 CIT-HSP-345
36	173.4	2.8	836	102	AO781745 HS-3122.A
37	173.2	2.8	413	10	A1355246 q74b06.x
38	173.2	2.8	430	13	A1859906 km33c01.x
39	173.2	2.8	508	100	A0632598 RPCI-11-4
40	173.2	2.8	784	101	AO738890 HS-5382.B
41	172.8	2.8	496	4	AA486819 ab19c10.r
42	172.8	2.8	624	96	AO373399 RPCI1-15
43	172.6	2.8	300	7	AA937809 nm98d02.s
44	172.4	2.8	397	10	A1417469 t433h09.x
45	172.4	2.8	439	14	A1961983 wt41a12.x

ALIGNMENTS

RESULT 1
A0057239

LOCUS A0057239 660 bp DNA GSS 30-JUL-1998
DEFINITION CIT-HSP-2340D14.TR CIT-HSP Homo sapiens genomic clone 2340D14, DNA sequence.
ACCESSION A0057239
VERSION A0057239.1 GI:3353765
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 660)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
TITLE Unpublished (1998)
JOURNAL Other-GSS: CIT-HSP-2340D14.TF
COMMENT Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@ligr.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.ligr.org/tldb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
FEATURES
source location/Qualifiers
1..660
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2340D14"
/clone_1id="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBel0AC11; site_1: HindIII; site_2: HindIII"
BASE COUNT 116 a 188 c 150 g 206 t
ORIGIN
Query Match 2.9%; Score 180.8; DB 88; Length 660;
Best Local Similarity 86.0%; Pred. No. 3.8e-22;
Matches 215; Conservative 0; Mismatches 27; Indels 8; Gaps 1;
Oy 1321 acctgagctcactgcaacctctgctcccaaggtcgaagcaattctctgtctcagctcc 1380
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 293 ATTCAGCTCAGTCAACCTCTGCTCCCGGTTCAAGCGATCTCCGTCTCAGCTCC 352
Oy 1381 cgcgtgagctggtgactacagcgc-----cagcccggtcaattttgtgtttgta 1432
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 353 CAAGTAGCTGGGATTACAGGCGCACACACACCGCCGGCTAATTTTGTATTTTGA 412
Oy 1433 gagatgggtttccacacattatgacccggtgtgtcttgaaacctggaacctcagtgatcca 1492
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 413 GAGATGGGCTTTCACACAGTGTGGCCAGGCTGCTCTCAACTCTGACTCTAGTGATCA 472
Oy 1493 cccacactcagctctctctaaagtctgggattacagagcatgagtcacgcgcgcgcgaagg 1552
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 473 CCCACCTGCTGCTCCCAAGTGTGGATTACAGGCTGCGGCACACGCGCCACCTAAT 532
Oy 1553 gtcaagtgttt 1562
||| |||||
Db 533 TTTGTATTT 542

DNA sequence.

ACCESSION A0379787
 VERSION A0379787.1 GI:4350810
 KEYWORDS GSS.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 539)
 Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.

REFERENCE

1 (bases 1 to 539)
 Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.

Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building

TITLE

Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building

JOURNAL

Unpublished (1997)
 Contact: Shaying Zhao, William Nierman, Mark Adams

COMMENT

Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208

Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page:

http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html

Seq primer: SP6
 Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..539

/organism="Homo sapiens"

/db_xref="GDB:7558034"

/db_xref="taxon:9606"

/clone="RPCI-11-152C3"

/clone_1lb="RPCI-11"

/sex="Male"

/cell_type="Lymphocytes"

/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"

116 t

1 others

123 g

112 c

187 a

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

2.9%; Score 179.8; DB 96; Length 539;

76.8%; Pred. No. 5.9e-22;

Conservative 0; Mismatches 63; Indels 8; Gaps 1;

1280 agggtaggggtctgtgtcttacacctaactgtatgtctacacctaagctcaactgaacc

327 AGAGTCTCGCTGTGACACAGGCTGGAGTTCAAGTGGCGGATCTGGCTCTCACTGAAC

1340 tctgtctcccaaggttcaagcaattctctgtctcagcctcccgctagctggagactacag

267 TCTGCTCCCGGGTTCAACCAATTCCTGCTCCAGCTCCCGAGTACGCTGGAGACACAG

1400 gc-----gaagcccggtcaattttgtattgtatgtatagatagatgggtttcaccata

207 GCATGTGCCACCATATCCCGCTAATTTTGTATTTTATAGTAAAGGGGTTTACACATG

1452 tagagcccggtgtgtgttgaactcctgaactcaggtatgatacaccacctaagctcctata

147 TTGGCCAGGCTGTCTTGAAGTCTGACCTCAAGTATATCACCAGCTTGGCTCTTAAG

1512 gtgtctggatctacagcatagatcaccggtcccggtcgaaggttcagttgttataaagaa

87 GTGCTGGGATTCAGACGTGATGACACACAGCCCGGCTCAATTCCTTTTAACTACTA

1572 taactt 1577

27 TGAATT 22

Db

RESULT 3

A036457 645 bp DNA GSS 17-JUN-1999
 A036457/c
 LOCUS
 DEFINITION RPCI-11-465121.t3 RPCI-11 Homo sapiens genomic clone RPCI-11-465121

ACCESSION A036457

VERSION A036457.1 GI:5099092

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 645)

Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.

Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building

Unpublished (1997)

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Fax: 301 838 0208

Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page:

http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html

Seq primer: SP6

Class: BAC ends.

Location/Qualifiers

1..645

/organism="Homo sapiens"

/db_xref="GDB:7678388"

/db_xref="taxon:9606"

/clone="RPCI-11-465121"

/clone_1lb="RPCI-11"

/sex="Male"

/cell_type="Lymphocytes"

/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"

174 t

139 g

118 c

214 a

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

2.9%; Score 179; DB 100; Length 645;

88.2%; Pred. No. 8e-22;

Conservative 0; Mismatches 20; Indels 8; Gaps 1;

1322 cctgtgctcaactgtcaactctgtctcccaaggttcaagcaattctctgtctcagctccc

248 CTTGAGCTACATGCAACCTCTGCTCCAGGTTCAAGTAATTCCTGCTCAGCTCC

1382 gcgtgtcgtggactcagggc-----caagcccggtcaattttgtattgtatgtatag

188 GAGTAGCTGGGATTCAGAGCGGTGTACACAGCCACCTAATTTTGTATTTTATAGT

1434 agatgggggtttacacatatgaacccggtgtgtgtgaactcctgaactcaggtgaactcac

128 AGATGGGATTTACCATATGTTGGCCAGGCTGTCTCCGACTCTGACTCAAGTATCTGC

1494 ccaactcagctcctaaagtgtgtgattacagcatagatcagccggtccggtccaa

68 CCACCTCAGGCTCCCAAGTGTGGATTAAGCATGAGCATGAGCAGCCGCGGCCAA

12

Db

RESULT 4

A0387027/c

LOCUS

DEFINITION

A0387027 678 bp DNA GSS 21-MAY-1999

RPCI11-153C12.t3 RPCI-11 Homo sapiens genomic clone RPCI-11-153C12,

Accession	DNA sequence.
A0387027	GSS.
A0387027.1	GI:4358050
KEYWORDS	
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 678)
AUTHORS	Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter ,J.C.
TITLE	Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
JOURNAL	Unpublished (1997)
COMMENT	Other GSS: RPCII-153C12 TV Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208 Email: hbe@tigr.org Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (piet@eijong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html Seq primer: SP6 Class: BAC ends. Location/Qualifiers 1..678 /organism="Homo sapiens" /db_xref="GDB:7558427" /db_xref="taxon:9606" /clone="RPCI-11-153C12" /clone_1fb="RPCI-11" /sex="Male" /cell_type="Lymphocytes" /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCII Human Male BAC Library"
BASE COUNT	210 A 151 C 171 G 146 T
ORIGIN	
Query Match	2.9% Score 179; DB 96; Length 678;
Best Local Similarity	77.4%; Pred No 7,9e-22;
Matches 233; Conservative	0; Mismatches 60; Indels 8; Gaps 1.
OY 1274	tccgtaggggtgaaggtctgtgtcctaacactaccctgtatgtcctaacacttgagtacctact 1333
Db 364	TCAGACGAGGTCTTCTGCTCTGTGCCTCAGCGCTGGAGTGCAATGGACAGATCTGGGCTCACT 305
OY 1334	gcacacctgtcctcccagggttcagaacaattctcccgctcccaagcctcccgctgaagcttgga 1393
Db 304	GCAACCTCCGCCCTCCAGGTTCAACAATTCTCTGCCCTCACACTCCCATGTGTAGCTGGGA 245
OY 1394	cacaaagc-----gcacgcgcgcgcgaattttgatattgttatagtagagatggggttic 1445
Db 244	TTACAGGACCACCCACCAACCAATGCCCGGCTTAATTTTTTATTTTAGTAGAGATGGGTTTC 185
OY 1446	accacattagcccgagctgtgtcttgaaactcctgaacctcaggtgatccacacacccctcacct 1505
Db 184	ACCATGTTGGCCAGGCTGTGTCTCGAAGCTCTTACCTCAGATGATCTGCCCGCTTAGCCT 125
OY 1506	cctaagatgctggagattacaagcatgatgtaccgcgcgccgcgaagggctcaagtgcttaatt 1565
Db 124	CCCAAGTGCTGGGATTTACAGGCGTGAGACCAACCGCGCCCTTATTTATTTATTTTAAAG 65
OY 1566	a 1566
Db 64	A 64

RESULT	5
LOCUS	AM978041 537 bp mRNA EST 02-JUN-2000
DEFINITION	EST390150 MAGE resequences, MAGO Homo sapiens cDNA, mRNA sequence.
ACCESSION	AM978041
VERSION	AM978041.1 GI:8169303
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	(bases 1 to 537)
JOURNAL	Hedge,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
COMMENT	,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
	Quackenbush,J.
	Assessment of gene expression patterns in a model of colon tumor
	metastasis using a 19,200 element cDNA microarray
	Unpublished (2000)
	Contact: John Quackenbush
	The Institute for Genomic Research
	9712 Medical Center Dr., Rockville, MD 20850, USA
	Tel: 301 838 3528
	Fax: 301 838 0208
	Email: johnq@tigr.org
	Plate: 387
FEATURES	Seq primer: Forward.
source	Location/Qualifiers
	1..537
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone_1lb="MAGE resequences, MAGO"
	/note="Vector: pBluescriptSKm"
BASE COUNT	119 a 157 c 141 g 118 t 2 others
ORIGIN	
Query Match	2.9%; Score 178.4; DB 25; Length 537;
Best Local Similarity	77.2%; Pred. No. 1e-21;
Matches 233; Conservative	0; Mismatches 61; Indels 8; Gaps 1;
Oy	1281 gggtgaagggtctgtgtcttacacactcatgtatgctctaacacctgagctcaactgaaacct 1340
Dd	6 GAGTCTTGCTGTGTTGCCACCGCTGGAGCTGCAGTGGCATGTCTCGCTCACTGCMAACT 65
Oy	1341 ctgcctcccaagttaagaacaatttcctcgtctcaagcccccgctgagcttggaactaagg 1400
Dd	66 CCACCTCCCACTTAATAAACGATTCTCCTGCTCAAGCTCCCGAGTAGCTGGGATTACAG 125
Oy	1401 cg-----cacggccgctaatttttgttatgtgttagtagagabgygggttaccatat 1452
Dd	126 TGCCCCACACCACACCCACCGACTAATTTTTTGTATTTTATAGATGAAGATGGGTTTCACATAT 185
Oy	1453 tagcccgctgtgtcttgtaacctctgtaacttaagtgatgatccaccacactaagctctctaag 1512
Dd	186 TGGCCAGACTGGTCTCGAACCTCTGACTCGAGTGATCACCCGCTTACGCTCCACAG 245
Oy	1513 tgctggaattacaagcatgagatcacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1572
Dd	246 TGCTTGGAATTATAGCGGTGAGCCACCGCGCCGCTTGAGGACAGAGTCTTAAAGAAG 305
Oy	1573 aa 1574
Dd	306 AA 307
RESULT	6
LOCUS	AO112451 516 bp DNA GSS 29-AUG-1998
DEFINITION	CIT-HSP-2372c9.TF CIT-HSP Homo sapiens genomic clone 2372c9, DNA
ACCESSION	AO112451
VERSION	AO112451.1 GI:3484611

KEYWORDS	GSS.
SOURCE	human.
ORGANISM	<i>Homo sapiens</i>
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Golden.K., 1 (bases 1 to 516)
AUTHORS	Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
TITLE	Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
JOURNAL	Unpublished (1998)
COMMENT	Other_GSS: CIT-HSP-2372C9.TR Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: mdadams@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tcdb/humgen/bac_end_search/bac_end_search.html . Seq primer: M13-21 Class: BAC ends.
FEATURES	Location/Qualifiers
source	1..516 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="2372C9" /clone_lib="CIT-HSP" /sex="Male" /cell_type="Sperm" /note="Vector: pBeloBAC11; site_1: HindIII; site_2: HindIII"
BASE COUNT	87 a 145 c 118 g 166 t
ORIGIN	
Query Match	2.9% Score 177.6; DB 89; Length 516;
Best Local Similarity	85.2%; Pred. No. 1,4e-21;
Matches 213; Conservative	0; Mismatches 29; Indels 8; Gaps 1
OY 1321	accgagctcactgcgaacctctgcctcccaaggttcgaagaattctctgctcgaagctcc 1380
DB 255	anctcagctcactgcgaacctctgcctcccggttcgaagaattctctgctcgaagctcc 314
OY 1381	cgcgtagctcgggaactaagcg-----caagcccggttaattttgtatgttagca 1432
DB 315	caagtagctcgggaatttacagcgccacacacacacgcccgcctaatTTTTTTATTTTAGTA 374
OY 1433	ggataggaggttcacacatatagccggagctgtgtctgaactcctgaccctcgaagtatca 1492
DB 375	gagatggggtttcacaccattttggccagcctggtctgaacctcttgaccttagtgatcca 434
OY 1493	ccacactcagcctctcctaagtgctggatatacagaagcatagtcacccgcgcgcgaag 1552
DB 435	cccaccttgccctcccaagaagtctggagatttacagcgcttgccacatgcgccacgctaat 494
OY 1553	gtcagtgatt 1562
DB 495	TTTTGCATT 504
RESULT 7	
AQ265389/c	577 bp DNA GSS 27-Oct-1998
LOCUS	CITBI-EI-2509010.TF CITBI-EI Homo sapiens genomic 2509010,
DEFINITION	DNA sequence.
ACCESSION	AQ265389
VERSION	AQ265389.1 GI:3793589
KEYWORDS	GSS.
SOURCE	human.

ORGANISM	Homo sapiens
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 577)
AUTHORS	Adams,M.D., Rounsley,S.D., Zhao,S., Baas,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Mable,C., Shizuya,H., Simon,M. and Venter,J.C.
TITLE	Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
JOURNAL	Unpublished (1998)
COMMENT	Other.GSs: CIRBI-El-2509010.TR Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: mdadams@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html. Seq primer: M13-21 Class: BAC ends.
FEATURES	Location/Qualifiers
Source	1..577 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="2509010" /clone_lib="CIRBI-El" /sex="male" /cell_type="sperm" /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI; Caltech Human BAC Library D"
BASE COUNT	167 a 127 c 137 g 146 t
ORIGIN	
Query Match	2.9%; Score 177.4; DB 91; Length 577;
Best Local Similarity	75.1%; Pred. No. 1.5e-21;
Matches 238; Conservative	0; Mismatches 71; Indels 8; Gaps 1;
QY	1321 acctgaagctcaatcgtgaacctcgtccctccaggttaagaacatctccgtccagccccc 1380
Db	368 ATCTGGGCTACATGGACACCTCTGCTCCACAGATTCAAGATCTTCCTCCACAGCTTC 309
QY	1381 cgcgtgagctggagaccacagggc-----gcacgcccggctaatttggatgttgatga 1432
Db	308 CGAGTATCTAGAGACTACAGGACACCCGCCACAGAGCTGGCTAATTTTGGTATTTTAGTA 249
QY	1433 ggaatgagggtttacacatatagaccggcgtgtgtcttgaacctcgtgaacctcaggatgcca 1492
Db	248 GAGAGGGGGTTTACCAATGTTGTGTGAGCGGTGATCTTGAACCTCGACCTCAGGCGATCCA 189
QY	1493 cccaccctcagccctctaaagtgtcgtggttaagaagcatgagatgcacccggccggcgcaagg 1552
Db	188 CCCGGCTTGGCTCCCAAGTGCTGGGATTAAGGCATGAGCCACTGCACCCAGCCAGCA 129
QY	1553 gtccagtgtttaaagaataaactggaatggttactaacaacacagaggaaacagacaaa 1612
Db	128 GATTAATTTTGTAAATCTAGACTGGAGTCACTGGACAGCTCTCTCAGGCAAAAGGAGAAAT 69
QY	1613 aagctgataaatttcag 1629
Db	68 AGTAATTAAGTGTATGAG 52
RESULT 8	
LOCUS	AI583291 548 bp mRNA EST 14-DEC-1999
DEFINITION	t556g02.x1 NC1 CGAP_HSC4 Homo sapiens cDNA clone IMAGE:224418 3'
ACCESSION	Similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN. ; contains Alu repetitive element; mRNA sequence.

VERSION	AT583291.1	GI:4569188
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryote: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	1 (bases 1 to 548)	
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
JOURNAL	Unpublished (1997)	
COMMENT	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert.Strausberg@nih.gov Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: David B. Kitzman, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www-bio.lnl.gov/bdnp/image/image.html Insert length: 664 Std Error: 0.00 Seq primer: -40UP from GIBCO High quality sequence stop: 464 POLYA-No.	

FEATURES	SOURCE
Location/Qualifiers	
1. 548	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone_1IMAGE:2244818"	
/clone_1ID="NCI-CGAP_HSC4"	
/tissue_type="CD34+ , CD38- from normal bone marrow donor"	
/lab_host="DH10B"	
/note="Organ: bone marrow; Vector: pMMP1; mRNA made from lymphoid tissue, cDNA made by oligo-dT priming. Directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, not-amplified. cDNA library Preparation: David B. Kitzman, Ph.D. Reference: Kitzman et al. (1996) Cancer Research 56:5380-5383."	
BASE COUNT	
150 a	136 c 129 g 133 t
ORIGIN	

Query Match	2.9%	Score 177.2;	DB 11;	Length 548;
Best Local Similarity	78.8%	Pred. No. 1,7e-21;		
Matches 227;	Conservative 0;	Mismatches 53;	Indels 8;	Gaps 1;
Qy 127	gtggaggtgaggtgtgtgtgtcttaacacttaactgtatgtcttaacaccgagctactca	1336		
Db 546	GAGGAGAGCTTGATCTGTGCTCAAGCGCTGAGATGCAAGTCATGATCTTGCTCACTTCA	487		
Qy 1337	acctctgcctcccaaggttcaagaacattccctgtctcagccctccgcgtaactgtgacta	1396		
Db 486	ACCTTCGGCTTCACAGGTTCACAGCAATTTCTGCTCCAGCTCCAGACACTGAGATA	427		
Qy 1397	cagcg-----cagcgccgctaatttgtatgttgtgtagagtgagtggtttacc	1448		
Db 426	CAGCGCCCCCGCCACACACCCCTGGCTAATTTTGTATTTTATGTAGAGTGGGTTTACC	367		
Qy 1449	atatiaagcccggtcgtgtcttgaacttcctgaaacctaggtgtaactcaaccacccaaactcct	1508		
Db 366	ATGTGGGCAAGCTGTGTGTGCACTCCAGACTCAGGTGATCAACCCACTTTGGTCTCC	307		
Qy 1509	aaagtgtctggtattacagatcagatcagtcacgcgcgcgcgcgaaggtca	1556		
Db 306	AAATGCTGTGGATTACAGCATGAGCCACCTGGCAGCGAGATTTA	259		

RESULT	9			
AO199435/c				
LOCUS	AO199435	434 bp	DNA	GSS
				20-APR-1999

DEFINITION	RPc111-58F5.TJ RPc11-11 Homo sapiens genomic clone RPc11-58F5, DNA sequence.
ACCESSION	AQ199435
VERSION	AQ199435.1
KEYWORDS	GI:3611634
SOURCE	GSS.
ORGANISM	human.
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE	1 (bases 1 to 434)
AUTHORS	Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P., and Venter,J.C.
TITLE	Use of human BAC End Sequences for Sequence-Ready Map Building
JOURNAL	Unpublished (1998)
COMMENT	Other_GSS: RPc111-58F5.TK

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@ligr.org
Clones are derived from the human BAC library RPC1-11. For BAC library availability, please contact Pieter de Jong (pieter@ligr.org, med.buffalo.edu). Clones may be purchased from BACpac Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics (info@resgen.com). BAC end search page: http://www.ligr.org/tldb/humgen/bac_end_search/bac_end_search.html
Class: BAC ends.

FEATURES	SOURCE	Location/Qualifiers
		1. 434
		/organism="Homo sapiens"
		/db_xref="GDB:7522012"
		/db_xref="taxon:9606"
		/clone="RPC1-11-58F5"
		/clone_11b="RPC1-11"
		/sex="Male"
		/cell_type="Lymphocytes"
		/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
		RPC111 Human Male BAC Library"
BASE COUNT		118 a 108 c 114 g 94 t
ORIGIN		

[illegible]

RESULT	10
LOCUS	AM979191
DEFINITION	AM979191 591 bp mRNA MRNA 02-JUN-2000 EST391301 MAGE resequences, MAGP Homo sapiens CDNA, mRNA sequence

ACCESSION	AM979191	GI:8170478
VERSION	AM979191.1	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.	
AUTHORS	1 (bases 1 to 591) Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and Quackenbush, J.	
TITLE	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray	
JOURNAL	Unpublished (2000)	
COMMENT	Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208 Email: johnq@igr.org Plate: 403 Seq primer: Forward.	
FEATURES	Location/Qualifiers	
source	1..591 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="MAGE Resequences, MAGE" /note="Vector: pBluescriptSKm"	
BASE COUNT	154 a 152 c 126 g 159 t	
ORIGIN		
Query Match	2.9%: Score 176.6; DB 25; Length 591;	
Best Local Similarity	71.9%: Pred. No. 2.1e-21;	
Matches	248: Conservative 0; Mismatches 89; Indels 8; Gaps 1	
OY	1281 gggtaagagctcgtgtcttaacacccctgtaagctcttaacactgagctctacgtcaacct 1340	
Db	132 GAGTTGTCCTGTGTCACCCAGGCTGAAGTGCACTGGCACAAATTCGGCTCAGCAACCT 191	
OY	1341 ctgcctccaggttcaagaatctctcgtctcaagctcccggtagctggagataagg 1400	
Db	192 CCACCTCCCAAGTTCAAGCAATTTCTGTCTCAGCCTCTTAAGTAGCTGGAGCTAGAG 251	
OY	1401 cgcacg-----ccggctaatcttctgtatgttagtagagatggyggttaccatat 1452	
Db	252 GGCCTGGCCACATACCAAGCTAATTTTCTATATTATTAGTAGAGATGGGGTTTCCACCATAT 311	
OY	1453 tagcccgagctgtcttgaactctctgaactcgaagtgatccaaccactcaagctctctaaag 1512	
Db	312 TGGTCAGGCTGGTCTTGAACCTCTGTACCTCAGGTGATCCACCCGCTTGGCTCTCCCAAG 371	
OY	1513 tctctggaatgaagataagatgaatcagcgcccgccgaagggatgaaggttcaataaggaat 1572	
Db	372 TCTCTGGGATGACAGGCGGTAGCGCAGCCGCCCAAGCAAGTTCTGGAAATTTTAAGCAA 431	
OY	1573 aactcgaatggttactaaacacacagggaaacagacaaagctg 1617	
Db	432 AATATTAATCTATTTAACACTCAATGGCATTTACTCAACAGAGATG 476	
RESULT 11		
AM273360	521 bp	03-JAN-2000
LOCUS	AM273360	
DEFINITION	xr38a04.x1 NCL_CCAP_Ut4 Homo sapiens cDNA clone IMAGE:2762382 3'	
ACCESSION	AM273360	
VERSION	AM273360.1	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;	

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 521)	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
	NCI-CCAP	http://www.ncbi.nlm.nih.gov/ncicgap.		
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
	Tumor Gene Index			
	Unpublished (1997)			
	Contact: Robert Strausberg, Ph.D.			
	Tel: (301) 496-1550			
	Email: Robert_Strausberg@nih.gov			
	Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.			
	Emmert-Buck, M.D., Ph.D.			
	cDNA Library Preparation: Life Technologies, Inc.			
	cDNA Library Arrayed by: Greg Lennon, Ph.D.			
	DNA Sequencing by: Washington University Genome Sequencing Center			
	Clone distribution: NCI-CCAP clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LNLW at:			
	www-bio.llnl.gov/bdpr/image/image.html			
FEATURES	source	1..521		
	Possible reversed clone: polyT not found			
	Seq primer: -40UP from GIBCO			
	High quality sequence stop: 411.			
	Location/Qualifiers			
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
	/clone="IMAGE:2762382"			
	/clone_1id="NCI-CCAP-Ut4"			
	/tissue_type="serous papillary carcinoma, high grade, 2			
	pooled tumors"			
	/note="Organ: uterus; Vector: PCMV-SPORT6; Site_1: SalI;			
	Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.			
	Average insert size 1.48 kb. Life Technologies catalog #:			
	11542-016"			
BASE COUNT	115 a	131 c	108 g	167 t
ORIGIN				
Query Match	2.9%	Score 176;	DB 21;	Length 521;
Best Local Similarity	80.7%;	Pred. No. 2.7e-21;		
Matches 221;	Conservative	0;	Mismatches 45;	Indels 8;
			Gaps 1;	
QY	1321	acctagctcaatgaaactctgcctcccaagtttaagcaatctctcgtctcaagctcc	1380	
DB	56	ATCTGGGCTCACTGCAACCTGCTCCCAAGTAAAGGATTCCTGCTCAGCCTCC	115	
QY	1381	cgcgttagcagacacagcg-----cagcgccgaattctgtatgttagta	1432	
DB	116	TGAGTAGCCAGGATTAACAGTGCCCGCCACACACACAGCAATTTTGTATTTAGTA	175	
QY	1433	gagatggggtttacacataatgacccggctgtgtcttgaaactctgcagctcagtgatcca	1492	
DB	176	GAGATGGGGTTCACTATGTTGGCCAGGCTAGTCTTGTACTCTGACCTCAGGTGATCCA	235	
QY	1493	cccacctaacgctctaaagtctggattacaggcatgagtcacccggcccgcccaag	1552	
DB	236	CCCGCTCAGCCTCCCAAGTGCTGGGATTAAGGCAATGACACCGCCCGGCTTTC	295	
QY	1553	gtcagtgtttaataaggaataactgtaattgtt	1586	
DB	296	CTGACTTTTGTAGTGAACCACTTCACTGATAT	329	
RESULT	12			
LOCUS	T53829	551 bp	mRNA	EST
DEFINITION	YB55DJ01.s1 StrataGene liver (#937224) Homo sapiens cDNA clone			
	sequence.			
ACCESSION	T53829			
VERSION	T53829.1	GI:655690		
KEYWORDS	EST.			
SOURCE	human.			

ORGANISM	Homo sapiens
REFERENCE	1 (bases 1 to 551)
AUTHORS	Walker, J., Lennon, G., Becker, M., Donald, M. F., Chappel, B., Haller, L., Dietrich, N., Dubuque, T., Faville, A., Gish, M., Hawkins, Chissey, S., Dietrich, N., Dubuque, T., Faville, A., Gish, M., Moore, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Maris, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellander, K., Soares, M. B., Tan, F., Thierly-Hegg, J., Trevisan, E., Underwood, R., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
TITLE	Generation and analysis of 280,000 human expressed sequence tags
JOURNAL	Genome Res. 6 (9), 807-828 (1996)
MEDLINE	97044478
COMMENT	Contact: Wilson R Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: estewatson.wustl.edu Insert Size: 760 High quality sequence stops: 380 Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 760 Std Error: 0.00 Seq primer: -21ml3 High quality sequence stop: 380.
FEATURES	Location/Qualifiers 1..551 /organism="Homo sapiens" /db_xref="GDB:497716" /db_xref="taxon:9606" /clone="IMAGE:77971" /clone_1b="Stratagene liver (#937224)" /sex="male" /dev_stage="49 years old" /lab_host="SOLR cells (kanamycin resistant)" /note="Organ: liver; Vector: pBluescript SK; Site 1: EcoRI Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT Hepatotomy from normal male caucasian. Average insert size: 1.1 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3' "
BASE COUNT	119 a 134 c 127 g 163 t 8 others
ORIGIN	
Query Match	2.9%; Score 176; DB 39; Length 551;
Best Local Similarity	80.7%; Pred. No. 2.7e-21;
Matches	221; Conservative 0; Mismatches 45; Indels 8; Gaps 1;
Db	131 accctgagctcagctgacacccctgctccaggttcaagcaatctctcgtctcagcctcc 1380
Db	47 ATCTCGGCTCACTCAACCTCTGCTCCAGATTCAAGCATTTCTCTGCTCAGCCTCC 106
Db	1381 cgcgttagctgagactaagcgc-----cagcccggttaatttttattgttagta 1432
Db	107 TGAATTAGCAGAGATTAAAGGTGCGCCGACACACCAACCAAGTAATTTTGTATTTTAA 166
Db	1433 gagaatgggtttcccaatattagcccgctgcttgaactctgagcccaagtgatca 1492
Db	167 GAGATGGGGTTTCTCTATGTTGGCCAGCTAGTCTTGTACTCTGTACCTCAGTGTATCA 226
Db	1493 cccacctcagcctctctaaagtgtctgagattacagagcatgagtcacgcgcgcgcacaag 1552
Db	227 CCCGCTCAGCCTCCCAAGTGTGGGATTACAGGATGTGATCAGCGCCCTGACCTTTC 286
Db	1553 gtccagttcttaataagaataacttgaaatgctt 1586
Db	287 CTGACTTTTATGATGATCACCATTCTACTGTAT 320
LOCUS	A0283440 589 bp DNA GSS 27-Apr-1999
DEFINITION	RPCL11-79G5.TJ RPCL11 Homo sapiens genomic clone RPCL11-79G5, DNA sequence.
ACCESSION	A0283440
VERSION	A0283440.1
KEYWORDS	GI:3908257
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	1 (bases 1 to 589)
AUTHORS	Mammalia, Eutheria: Primates; Catarrhini: Homnidae; Homo.
TITLE	Unpublished (1998)
JOURNAL	Other_GSSs: RPCL11-79G5.TJ
COMMENT	Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: mdadams@tigr.org Clones are derived from the human BAC library RPCL11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.bufileo.edu). Clones may be purchased from BACPRC Resources (http://bacpac.med.bufileo.edu/ordering) or from Research Genetics (Info@resgen.com). BAC end search page: http://www.tigr.org/ldb/hungen/bac_end_search/bac_end_search.html Seq primer: SP6 Class: BAC ends.
FEATURES	Location/Qualifiers 1..589 /organism="Homo sapiens" /db_xref="GDB:7530100" /db_xref="taxon:9606" /clone="RPCL11-79G5" /clone_1b="RPCL11" /sex="Male" /cell_type="Lymphocytes" /note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; RPCL11 Human Male BAC Library"
BASE COUNT	146 a 126 c 136 g 181 t
ORIGIN	
Query Match	2.8%; Score 175.8; DB 91; Length 589;
Best Local Similarity	75.7%; Pred. No. 2.9e-21;
Matches	234; Conservative 0; Mismatches 67; Indels 8; Gaps 1;
Db	1280 agagtgaggtctgctgtctctacacccactctgtatgctctacaccgcagactcagcgaac 1339
Db	105 AGAATCTTGTCTGTGTGGCCAGCTGAGTACAGTGTGCGATGTCACTCTCACTCAACC 164
Db	1340 tctgacctccaggttlaagcaattccctgcttcagcctcccggttagctgagactaag 1399
Db	165 TCTGACTCTGTGGTTCAGCAATTCCTGTGTAGCCCCCGAGTACTGGGATTACAG 224
Db	1400 ggc-----cagcccggttaattttgtattgtagtagaagtggtttcacata 1451
Db	225 GTGCTCCACACATGCCCTAGCTAATTTTGTATTTTATAGACAGATGGGTTTACCAT 284
Db	1452 ttaagcccgctgtcttgaactctgactcaggtatgataccacccactcagcctctaa 1511
Db	285 TTGGTCAAGCTGTGTAAGTCTGACTCTGATGTGATCACCCTCTCAGCTCCCAA 344
Db	1512 gtctgtgagattacagcatagatcacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1571
Db	345 GTGCTGGGATTACAGGCGTGAGCCACCGTGTGCTGCGAGGGGTATTTTATAGGAA 404
Db	1572 taacttga 1580
Db	405 TAATCTGCA 413


```

RESULT 14
LOCUS      AQ474222/c
DEFINITION
ACCESSION  AQ474222
VERSION    AQ474222
KEYWORDS   GSS.
SOURCE     human.
ORGANISM   Homo sapiens
            Homo sapiens
            Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE  1 (bases 1 to 366)
AUTHORS    Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
            Venter,J.C.
TITLE      Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
            Map Building
            Unpublished (1997)
JOURNAL    Other GSSs: CITBI-E1-2601E18.TF
COMMENT    Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbeetlgr.Org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/cdb/hungen/Bac_end_search/Bac_end_search.html.
            Seq primer: M13 Reverse
            Class: BAC ends.

```

FEATURES	SOURCE	Location/Qualifiers
	1. .385	/organism="Homo sapiens"
		/db_xref="taxon:9606"
		/clone="2601E18"
		/clone_1b="CITR1-E1"
		/sex="male"
		/cell_type="sperm"
		/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI; Calnech Human BAC Library D"
BASE COUNT	88 a	104 c 116 g 78 t
ORIGIN		

Query Match	2.8%	Score 175.4	DB 98	Length 386
Best Local Similarity	76.9%	Pred. No. 3,6e-21		
Matches 230	Conservative	0	Mismatches 61	Indels 8
				Gaps 1
Oy 1281	gggtgaggtctgctgtctacacctaactgtatgctctaacctcagctcaactgcaact	1340		
Db 379	gagctctctctgctgcgccacgctaagcagtgacagcacaatctgcgctcactgcgaagt	320		
Oy 1341	ctgctcccaagttcaagaattctccctctccacagctcccgctagctcggaactaag	1400		
Db 319	ctgctctccgggcttacgcatttctctctcctcctcagcctccagagtaacgggactacag	260		
Oy 1401	cgc-----acgcgcggtcaatttctgtatgttagtaagaaatggggtttacatat	1452		
Db 259	cgctgcgcacacgcgcgcgcctattttttattttatgagacacagggatttaccgtgt	200		
Oy 1453	tggccgcgctgttcttgaaactctctgaacctcaagttgataccaccacactcaagcctcaag	1512		
Db 199	tagccagagatgcttgagattctctgtaacctcactgaagtatccgcccgcctcactttcccaag	140		
Oy 1513	tgcctggaattacaagcattgatacgcgcgcgcgcgaaggtgcagtgtttaataagaa	1571		
Db 139	tctctggattacaggcggtgagccacgcgcgcgcctatttttttataaacagaaa	81		

LOCUS	AO415030/c				
DEFINITION	AO415030	711 bp	DNA	GSS	23-MAR-1999
ACCESSION	RPCI-11-203E3.TV	RPCI-11 Homo sapiens genomic clone	RPCI-11-203E3,		
VERSION	AO415030				
KEYWORDS	DNA sequence.				
SOURCE	AO415030.1	GI:4473999			
ORGANISM	GSS.				
REFERENCE	human.				
AUTHORS	Homo sapiens				
TITLE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo. 1 (bases 1 to 711)				
JOURNAL	Zhao,S., Adams,M.D., Niernan,W., Malek,J., de Jong,P. and Venter,J.C.				
COMMENT	Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building				
	Unpublished (1997)				
	Other-GSSs: RPCI-11-203E3.TJ				
	Contact: Shaying Zhao, William Niernan, Mark Adams				
	Department of Eukaryotic Genomics				
	The Institute for Genomic Research				
	9712 Medical Center Dr., Rockville, MD 20850				
	Tel: 301 838 0200				
	Fax: 301 838 0208				
	Email: hdbet@tigr.org				
	Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Plieter de Jong (plieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tldb/humgen/bac_end_search/Bac_end_search.html.				
	Seq primer: T7				
	Class: BAC ends.				

FEATURES	SOURCE	location/Qualifiers
		1..711
		/organism="Homo sapiens"
		/db_xref="GDB:757766"
		/db_xref="taxon:9606"
		/clone="RPC1-11-203E3"
		/clone_1lb="RPC1-11"
		/sex="Male"
		/cell_type="Lymphocytes"
		/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI"
		RPC11 Human Male BAC Library"
BASE COUNT		270 a 150 c 141 g 150 t
ORIGIN		

[illegible]

Db 65 CTTCTCTGCTTTCGTA 48

Search completed: December 3, 2000, 10:15:26
Job time: 14004 sec

• • • •

